GOVERNMENT OF INDIA
SCIENCE AND TECHNOLOGY
LOK SABHA

UNSTARRED QUESTION NO:5186
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GENOME MAPPING OF CROPS
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Will the Minister of SCIENCE AND TECHNOLOGY be pleased to state:

(a) whether Indian scientists have started work on genome mapping, expression sequence tags and genetic variability of various crops;

(b) if so, the details thereof; and

(c) the extent to which these new varieties will increase the production of crops?

Answer

MINISTER OF THE STATE IN THE MINISTRY OF SCIENCE & TECHNOLOGY AND MINISTER OF EARTH SCIENCES (KAPIL SIBAL)

(a) Yes, Sir. Indian Scientists have started work on genome mapping, expression sequence tags (ESTs) and genetic variability of various crops like rice, wheat, chickpea, tomato, sugarcane and coffee.

(b) Indian scientists have participated in the International Rice Genome Sequencing Project (IRGSP). IRGSP sequenced 370 million bases of rice genome and scientists from ten nations participated in it. The Indian scientists have successfully decoded the genome information of the rice chromosome number 11 as part of the IRGSP. The rice genome has been shown to have 37,544 genes, out of which 1443 have been identified in the region sequenced by Indian Scientists. This is being followed by functional genomics programme in Rice. India is also participating in international tomato genome sequencing project for the sequencing of tomato chromosome 5 once again under an international consortium of ten countries.

At University of Delhi South Campus, New Delhi, scientists have generated about 25000 ESTs in sugarcane and about 4000 ESTs in wheat. The sugarcane ESTs have been used to develop markers in sugarcane to map agronomically useful traits at IARI, New Delhi. The International Centre for Genetic Engineering and Biotechnology (ICGEB), New Delhi has developed ESTs from pearl millet. In tomato, root-specific ESTs are being developed at MKU, Madurai. In addition, some progress on mapping in tomato has been made for virus and bacterial wilt resistance under tomato genome initiative. The National Centre for Plant Genome Research (NCPGR) has undertaken studies on comparative genomics with focus on wheat, foxtail millet, tomato, chilies, Medicago and Brassica and could map QTLs for grain weight for wheat. The Centre is also working on Genome structure analysis in chickpea and Catharanthus roseu.

Eleven STMS markers have been developed from Cicer reticulatum, the wild progenitor of chickpea,and used to study the inter-specific polymorphism in Cicer sps. The National Bureau of Plant Genetic Resources (NBPGR), New Delhi has been working on genetic diversity studies in various crops of importance to India since 1996. It has so far analyzed released varieties in more than 33 different crops plants. In addition, elite landraces and germplasm lines of these crops have also been analyzed. Besides, studies on crop diversity and domestication have been conducted in brinjal, mung/urd/ricebean and their wild relatives, horsegram, sesame, buckwheat, Himalayan barley landraces, fingermillet, rice landraces etc., which have helped in identifying the extent and distribution of diversity in these crops.

(c) The decoded genome information of crops after mapping could play a pivotal role in the rapid discovery of new gene functions and DNA markers for the development of improved varieties through molecular breeding. The new varieties are likely to break the yield plateau that has been now reached through conventional breeding efforts. However, at this stage it is difficult to quantify the increase in production but future varietal improvement program would definitely benefit from these research efforts.